

FIGURE 1

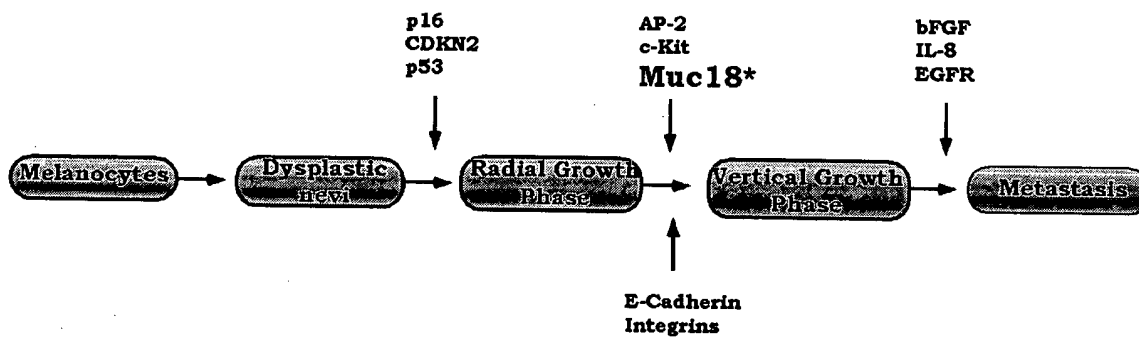


FIGURE 2

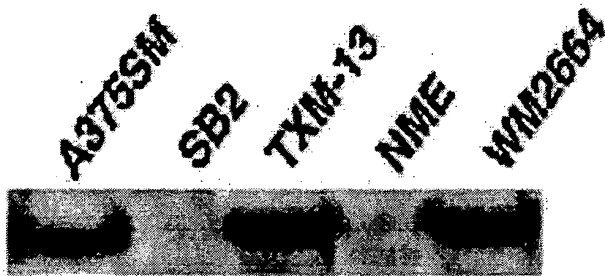


FIGURE 3

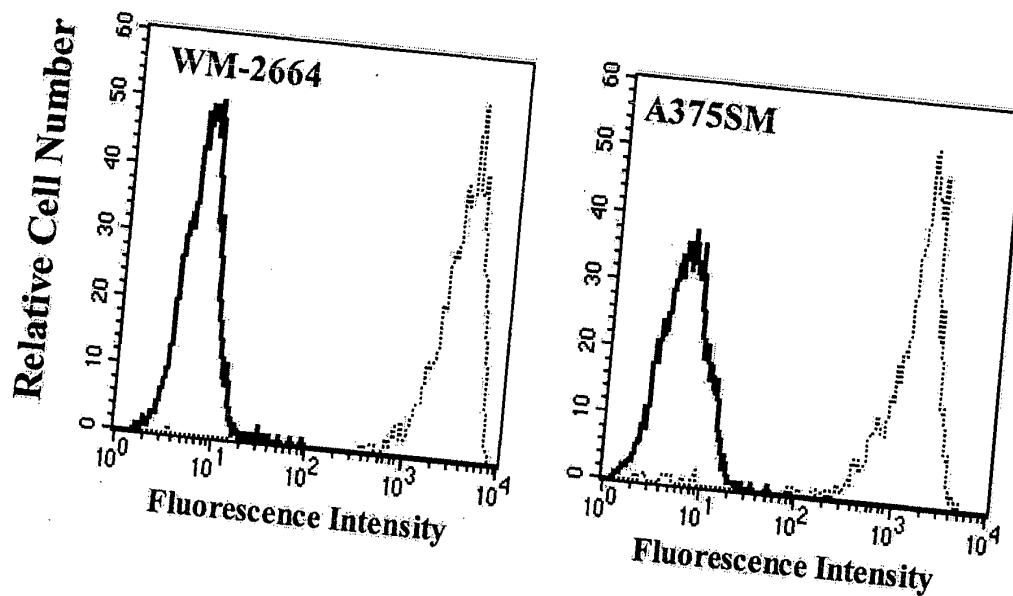


FIGURE 4

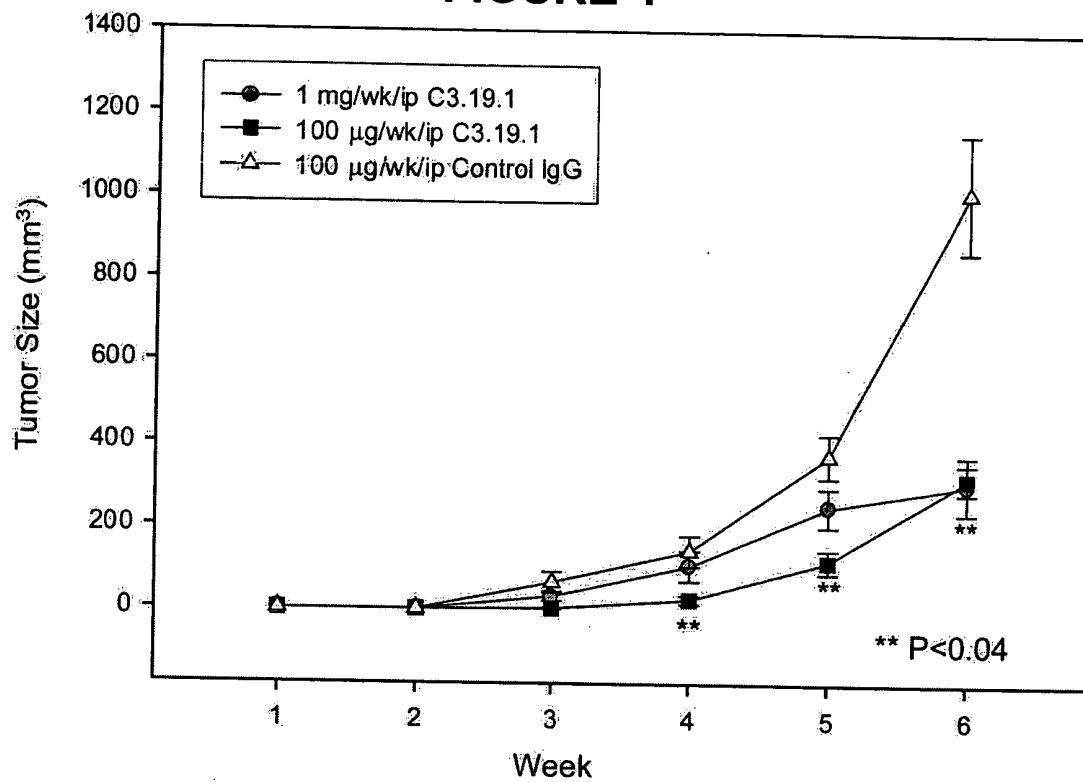


FIGURE 5

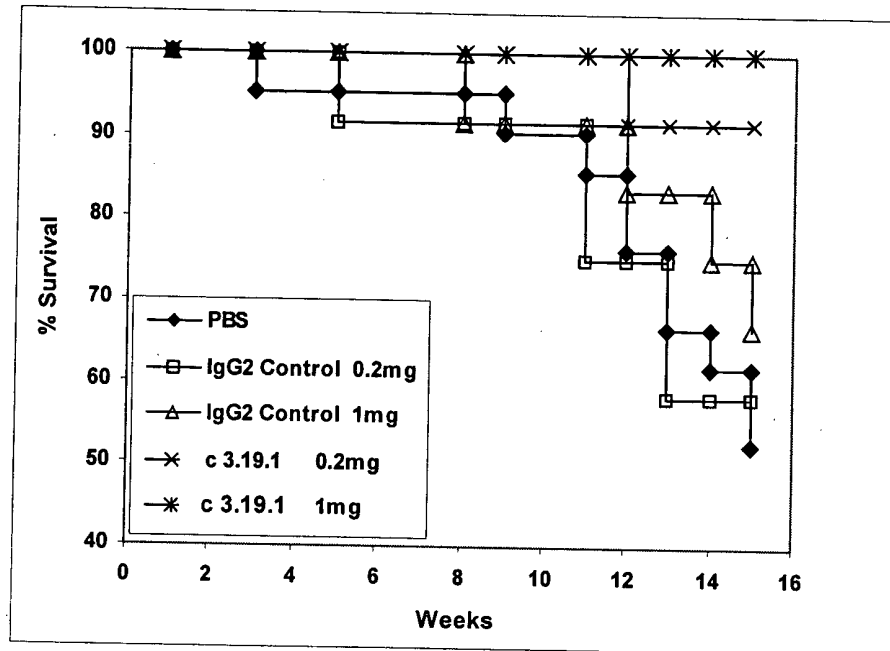


FIGURE 6

ANTI-MUC18 ANTIBODY C3.19.1

Nucleotide Sequence of heavy chain variable region

5' -

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGCTATATCTATTACACTTGGACCTCCAACCTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTGGACACGTCCAAAACAGTTCTCCCTGAGGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTTTATTACTGTGCGAGAGATCAGGGGACAGTGGTTACTACCCGATGCTTTTGATATC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG 3' (SEQ ID NO: 3)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWSNYPNPSLKSR
VTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMTVTVSS (SEQ ID
NO: 1)

Nucleotide Sequence of light chain variable region

5' -

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC
TGCAGGTCTAGTCAGAGCCTCCTGCGTAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAG
CCAGGACAGTCTCCACATCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGG
TTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAGCTCAACAAAGTCCGATCACCTTCGGCCAAGGGACACGACTGGAG
ATTAAAC 3' (SEQ ID NO: 4)

Amino Acid Sequence of Light Chain Variable Region

DIVMTQSPLSLPVTPGEPASISCRSSQSLLRNNGYNYLDWYLQKPGQSPHLLIYLGSNRASGVDPDR
FSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGRLEIK (SEQ ID NO: 2)

FIGURE 7

ANTI-MUC18 ANTIBODY C6.11.13

Nucleotide Sequence of heavy chain variable region

5' -
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGGGGGAGATGGCTACAAGTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG-3' (SEQ ID NO: 7)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYSGSTYYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKWGQGLTVTVSS (SEQ ID NO:
5)

Nucleotide Sequence of light chain variable region

5'
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTAGCAACAACCTTAGCCTGGTATCAGCAGAAACCTGGCCAGGCTCCC
AGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAAGTGGCAGTGGG
TCTGGGACAGAGTTCCTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGT
CAGCAGTATAATAACTGGCCTCGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAAC 3'
(SEQ ID NO: 8)

Amino Acid Sequence of Light Chain Variable Region

EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG
SGTEFTLTISLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK (SEQ ID NO: 6)

FIGURE 8

ANTI-MUC18 ANTIBODY C3.10

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCAC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGCT CTGTGACCGC TCGGACACG GCCCTTTATT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 11)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY IYYTWTNIN
61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT ALYYCARDQG QWLLPDAFDI WQGTMVTVS
121 S (SEQ ID NO: 9)
```

Nucleotide Sequence of light chain variable region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GAGCATTAGC AACTATTTAA ATTGGTATCA GCAGAAACCA
121 GGAAAAGCCC CTAAGCTCCT GATCTATGGT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCACTG GCAGTGGATC TGGGACAGAT TCACTCTCA CCATCAGCAG TCTGCAACCT
241 GAAGATTTTG CAACCTACTA CTGTGACAG AGTTACAGTA CCCCTCCGGA GTGCAGTTTT
301 GGCCAGGGGA CCAAGCTGGA GATCAAAC (SEQ ID NO: 12)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQSIG NYLNWYQQKP GKAPKLLIYG ASSLQSGVPS
61 RFSGSGSGTD FTLTISSLQP EDFATYYCRQ SYSTPPECSF GQGTKLEIK (SEQ ID NO:
10)
```


FIGURE 9

ANTI-MUC18 ANTIBODY C3.22

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTACAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTGGTT ACTACTGGAC TTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTTCATCT ATTACAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAGTTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACTGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGAG
301 GGAGATGGCT TTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG (SEQ ID
NO: 15)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGYYWTWIR QHPGKGLEWI GFIIYSGSTY
61 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARE GDGFDYWGQG TLVTVSS (SEQ
ID NO: 13)
```

Nucleotide Sequence of light chain variable region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTACGCG GCAGTGGATC TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGCTCAC TTTCGGCGGA
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 16)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVIT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPLTFGG GTKVEIK (SEQ ID NO: 14)
```

FIGURE 10

ANTI-MUC18 ANTIBODY C3.27

Nucleotide Sequence of heavy chain variable region

1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCTC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGTT CTGTGACCGC TGGCGACACG GCCGTTTACT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 19)

Amino Acid Sequence of Heavy Chain Variable Region

1 QVQLQESGPG LVKPSSETLSL TCTVSGGSIS SYIWSWIRQP PGKGLEWIGY IYYTWTSNYN
61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT AVYYCARDQG QWLLPDAFDI WGQGTMTVTS
121 S (SEQ ID NO: 17)

Nucleotide Sequence of light chain variable region

1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTTCAGCG GCAGTGGATC TGGGACAGAG TTTACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGTGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 20)

Amino Acid Sequence of Light Chain Variable Region

1 DIQMTQSPSS LSASVGDRTV ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPWTFGQ GTKVEIK (SEQ ID NO: 18)

FIGURE 11

ANTI-MUC18 ANTIBODY C3.45

Nucleotide Sequence of heavy chain variable region

```
1 CAGG TTCAGC TGGTGCAGTC GGGAGCTGAG GTGAAGAAGC CTGGGGCCTC AGTGAAGGTC
61 TCCTGCAAGG CTTCTGGTTA CACCTTTTTT AGCTATGGTT TCAGCTGGGT GCGACAGGCC
121 CCTGGACAAG GGCTTGAGTG GCTGGGATGG ATCAGCGCTT ACAATGGTAA CACAAACTAT
181 GCACAGAAGC TCCAGGGCAG AGTCACCATG ACCACAGACA CTTCACGAG CACAGCCTAC
241 ATGGAGCTGA GGAGCCTGAG ATCTGACGAC ACGGCCGTGT ATTACTGTGC GAGAGAAACT
301 AAGG TTCGGG GAGTCCACTA CTACGGTATG GACGTCTGGG GCCAAGGGAC CACGGTCACC
361 GTCTCCTCAG (SEQ ID NO: 23)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLVQSGAE VKKPGASVKV SCKASGYTFF SYGFSWVRQA PGQGLEWLGW ISAYNGNTNY
61 AQKLQGRVTM TTDSTSTAY MELRSLRSDD TAVYYCARET KVRGVHYYGM DVWGQGTIVT
121 VSS (SEQ ID NO: 21)
```

Nucleotide Sequence of light chain variable region

```
1 DIVMTQSPDS LAVSLGERAT IICKSSQSIL YSSNNKNYLG WYQQKPGQPP KLLIYWASTR
61 ESGVPARFSG SGSGTDFTLT INSLQAEDVA VYYCQYYST PRSFGQGTMV EIK (SEQ ID
NO: 24)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT CTCTGGGCGA GAGGGCCACC
61 ATCATCTGCA AGTCCAGCCA GAGTATTTTA TACAGCTCCA ACAATAAGAA CTACTTAGGT
121 TGGTACCAGC AGAAACCAGG ACAGCCTCCT AAGCTGCTCA TTTACTGGGC ATCTACCCGG
181 GAATCCGGGG TCCCTGCCCC ATTCA GTGCG AGCGGGTCTG GGACAGATTT CACTCTCACC
241 ATCAACAGCC TGCAGGCTGA AGATGTGGCA GTTTATTACT GTCAGCAATA TTATAGTACT
301 CCTCGGTCGT TCGGCCAAGG GACCATGGTG GAAATCAAAC (SEQ ID NO: 22)
```

FIGURE 12

ANTI-MUC18 ANTIBODY C3.65

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTACAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAAC AGTGGTGGTT GCTACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTACATCT ATTCCAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAATTACC TTATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAAGTCTAT GACTGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGAT
301 CGGGAAACAG CTGGTTTTGA CTACTGGGGC CAGGGAACCC TGGTCACCGT CTCCTCAG (SEQ
ID NO: 27)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSQTLST TCTVSGGSIN SGGCYWSWIR QHPGKGLEWI GYIYSSGSTY
61 YNPSLKSRIT LSVDTSKNQF SLKLNSMTAA DTA VYYCARD RETAGFDYWG QGTLVTVSS
(SEQ ID NO: 25)
```

Nucleotide Sequence of light chain variable region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC AGGCGAGTCA GGACATTAAC AACTATTTAA ATTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCTCCT GATCTACGAT GCATCCAATT TGGAAACAGG GGTCCCATCA
181 AGGTTTCAGTG GAAGTGGATC TGGGACAGAT TTTACTTTCA CCATCAGCGG CCTGCAGCCT
241 GAGGATATTG CAACATATTA CTGTCAACAG TATGATACTC TCCCTCTCAC TTTCGGCGGC
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 28)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCQASQDIN NYLNWYQQKP GKAPKLLIYD ASNLETGVPS
61 RFSGSGSGTD FTFTISGLQP EDIATYYCQQ YDTLPLTFGG GTKVEIK (SEQ ID NO: 26)
```

FIGURE 13

ANTI-MUC18 ANTIBODY C6.1

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGGTGGAGTC GGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC
61 TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGCTATGCCA TGCACTGGGT CCGCCAGGCT
121 CCAGGCAAGG GGCTGGAGTG GGTGGCAGTT ATATCATATG ATGGAAGTAA TAAATACTAT
181 GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT
241 CTGCAAATGA ACAGCCTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGATCGATT
301 TTTGGAGTGG TTATCGACTA CGGTATGGAC GTCTGGGGCC AAGGGACCAC GGTCACCGTC
361 TCCTCAG (SEQ ID NO: 31)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV ISYDGSNKYY
61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARSI FGVVIDYGMD VWGQGTTVTV
121 SS (SEQ ID NO: 29)
```

Nucleotide Sequence of light chain variable region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCGAGTCA GGGCATTAGA AATTATTTAG CCTGGTATCA GCAGAATCCA
121 GGGAAAGTTC CTAAGCTCCT GATCTATGGT GCATCCACTT TGCAATCAGG GGTCCCATCT
181 CGGTTCAAGT GCAGTGGATC TGGGACAGAT TTTACTCTCA CCATCAGCAG CCTGCAGCCT
241 GAAGATGTTG CAACTTATTA CTGTCAAAAG TTTAGCAGTC CCCCATTAC TTTTCGGCCCT
301 GGGACCAAAG TGGATATCAG TC (SEQ ID NO: 32)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQNP GKVPKLLIYG ASTLQSGVPS
61 RFSGSGSGTD FTLTISSLQP EDVATYYCQK FSSPPFTFGP GTKVDIS (SEQ ID NO: 30)
```

FIGURE 14

ANTI-MUC18 ANTIBODY C6.9

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGGAGCAGTC GGGGCCAGGA CTGGTGAAGC CTCAGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTACTT ACCACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAGGGGCCT GGAGTGGATT GGATACATCT ATTACAGTGG GAGCACCTAC
181 CACAACCCGT CCCTCAAGAG TCGAATTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACGGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGGG
301 GGAGATGGCT ACAGATACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG (SEQ ID
NO: 35)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLEQSGPG LVKPSETLSL TCTVSGGSIS SGTYHWSWIR QHPGRGLEWI GYIYYSGSTY
61 HNP SLKSRIT ISVDTSKNQF SLKLSSVTAA DTA VYYCARG GDGYRYWGQG TLVTVSS (SEQ
ID NO: 33)
```

Nucleotide Sequence of light chain variable region

```
1 GAAATAGTGA TGACGCAGTC TCCAGCCACC CTGTCTGTGT CTCCAGGGGA AAGAGCCACC
61 CTCTCCTGCA GGGCCAGTCA GAGTATTAGC AACAACTTCG CCTGGTACCA GCAGAAACCT
121 GGCCAGGCTC CCAGGCTCCT CATCTTTGGT GCATCCACCA GGGCCACTGG TATCCCAGCC
181 AGGTT CAGTG GCAGTGGGTC TGGGACAGAA TTCACTCTCA CCATCAGCAG CCTACAGTCT
241 GAAGATTTTG CAGTTTATTA CTGTCAGCAG TATAATAACT GGCCTCGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 36)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 EIVMTQSPAT LSVSPGERAT LSCRASQ SIS NNFAWYQQKP GQAPRLLIFG ASTRATGIPA
61 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPRTFGQ GTKVEIK (SEQ ID NO: 34)
```

FIGURE 15

ANTI-MUC18 ANTIBODY C6.2

Nucleotide Sequence of heavy chain variable region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CCTCGGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT ACTTACTACT GGAGTTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGATAC ATCTATTACA CTGGGAACAC CTACTACAAC
181 CCCTCCCTCA AGAGTCGAGT CACCGTTTCA GTTGACACGT CCAAGAACCA GTTCTCCCTG
241 AAGCTGAACT CTGTGACCGC TCGGACACG GCCGTGTATT ACTGTGCGAG AGATCCAGGC
301 CAGTGGCTGG TCCCTGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CTCCGTCTCT
361 TCAG (SEQ ID NO: 39)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS TYYWSWIRQP PGKGLEWIGY IYYTGNTYYN
61 PSLKSRVTVS VDTSKNQFSL KLNSVTAADT AVYYCARDPG QWLVPDAFDI WGQGTMTSVS
121 S (SEQ ID NO: 37)
```

Nucleotide Sequence of light chain variable region

```
1 GATATTGTGA TGA CTCTAGTC TCCACTCTCC CTGCCCCGTCA TTCCTGGAGA GCCGGCCTCC
61 ATCTCCTGCA GGTCTAGTCA GAGCCTCCTG CAGAGTAATG GAAACAAC TAATCGGGCC
121 TACCTGCAGA AGCCAGGGCA GTCTCCACAG CTCCTGATCT ATTTGGGTTC TAATCGGGCC
181 TCCGGGGTCC CTGACAGGTT CAGTGGCAGT GGATCAGGCA CAGATTTTAC ACTGAAAATC
241 AGCAGAGTGG AGGCTGACGA TGTGTTGGATT TATTACTGCA TGCAAGCTCT CCAAATTCCT
301 CTCACCTTCG GCGGAGGGAC CAAGGTGGAG ATCAAAC (SEQ ID NO: 40)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIVMTQSPLS LPVIPGEPAS ISCRSSQSLL QSNNGNYYLDW YLQKPGQSPQ LLIYLGSNRA
61 SGVPDRFSGS GSGTDFTLKI SRVEADTVGI YYCMQALQIP LTFGGGTKVE IK (SEQ ID
NO: 38)
```

FIGURE 16

positives: 79,3%	identity: 76,0%
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Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

		Section 1
	(1) 1 10 20 30 40 53	
A15-3.10_LC	(1) DIQMTQSPSSLSASVGRVTITCRASQSISYLNWYQQKPGKAPKLLIYGASS	
O2	(1) DIQMTQSPSSLSASVGRVTITCRASQSISYLNWYQQKPGKAPKLLIYAASS	
Consensus	(1) DIQMTQSPSSLSASVGRVTITCRASQSIS YLNWYQQKPGKAPKLLIYAASS	
		Section 2
	(54) 54 60 70 80 90 106	
A15-3.10_LC	(54) LQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQSYSTPECSFGQGTKL	
O2	(54) LQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQSYSTP-----	
Consensus	(54) LQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYC QSYSTP	
		Section 3
	(107) 107	
A15-3.10_LC	(107) EIK	
O2	(96) ---	
Consensus	(107)	

positives: 85.3%	identity: 84.4%
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USE OF ANTIBODIES AGAINST THE MUC18 ANTIGEN

Bar-Eli et al.

Appl. No.: Not Assigned Atty Docket: ABGENIX.030CI

FIGURE 18

								Section 1
	(1)	1	10	20	30	40	53	
A15-3.22_HC	(1)	QVQLQESGPGGVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI						
VH4-31	(1)	QVQLQESGPGGVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI						
Consensus	(1)	QVQLQESGPGGVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI						
								Section 2
	(54)	54	60	70	80	90	106	
A15-3.22_HC	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR						EGDGFDFY
VH4-31	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR						-----
Consensus	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR						
								Section 3
	(107)	107	117					
A15-3.22_HC	(107)	WGQGTIVTVSS						
VH4-31	(100)	-----						
Consensus	(107)							

Positives: 84.6% Identity: 82.9%

FIGURE 19

										Section 1
	(1)	1	10	20	30	40	50	60	70	53
A15-322_LC	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASS								
A30	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASS								
Consensus	(1)	DIQMTQSPSSLSASVGDRVTTTCRASQGIKNDLGWYQKPGKAPKRLIYAASS								
										Section 2
	(54)	54	60	70	80	90	100	110	120	106
A15-322_LC	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----								
A30	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP-----								
Consensus	(54)	LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLOHNSYP								
										Section 3
	(107)	107								
A15-322_LC	(107)	K								
A30	(96)	-								
Consensus	(107)									

Positives: 88.8% Identity: 88.8%

USE OF ANTIBODIES AGAINST THE MUC18 ANTIGEN

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Appl. No.: Not Assigned Atty Docket: ABGENIX.030C1

FIGURE 21

		Section 1						
		(1)	1	10	20	30	40	53
A15-3.27	LC	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGMVQKPKKAPKRLIYAASS					
	A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGMVQKPKKAPKRLIYAASS					
	Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIKNDLGMVQKPKKAPKRLIYAASS					
		Section 2						
		(54)	54	60	70	80	90	106
A15-3.27	LC	(54)	LQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCLQHNSYF					
	A30	(54)	LQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCLQHNSYF					
	Consensus	(54)	LQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCLQHNSYP					
		Section 3						
		(107)	107					
A15-3.27	LC	(107)	K					
	A30	(96)	-					
	Consensus	(107)						

Positives: 88.8% Ident: 88.8%

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FIGURE 22

						Section 1
						(1) 1 10 20 30 40 53
A15-3.45_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGF				SWVRQAPGGGLEWIGWISA
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGF				SWVRQAPGGGLEWIGWISA
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF				SYG SWVRQAPGGGLEWIGWISA
						Section 2
						(54) 54 60 70 80 90 106
A15-3.45_HC	(54)	YNGNTNYAQKLGGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVH				
VH1-18	(54)	YNGNTNYAQKLGGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR				-----
Consensus	(54)	YNGNTNYAQKLGGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR				
						Section 3
						(107) 107 123
A15-3.45_HC	(107)	YYGMDVWGQGTITVTVSS				
VH1-18	(99)	-----				
Consensus	(107)					

positives: 78.0% identity: 77.2%

FIGURE 23

										Section 1
	(1)	1	10	20	30	40	50	60	70	53
A15-3.45_LC	(1)	DIVMTQSPDLSLAVSLGERATTICKSSQSILYSSNNRNYLGWYQOKPGQPPKLL								
B3	(1)	DIVMTQSPDLSLAVSLGERATTICKSSQSILYSSNNRNYLGWYQOKPGQPPKLL								
Consensus	(1)	DIVMTQSPDLSLAVSLGERATTICKSSQSILYSSNNRNYLGWYQOKPGQPPKLL								
										Section 2
	(54)	54	60	70	80	90	100	110	120	106
A15-3.45_LC	(54)	IYWASTRESGVPARTSGSGSGTDFTLTINSIQAEDVAVYYCQYYSTERSFGQ								
B3	(54)	IYWASTRESGVPDRFSGSGSGTDFTLTINSIQAEDVAVYYCQYYSTERSFGQ								
Consensus	(54)	IYWASTRESGVPARTSGSGSGTDFTLTINSIQAEDVAVYYCQYYSTERSFGQ								
										Section 3
	(107)	107	113							
A15-3.45_LC	(107)	GTMVEIK								
B3	(102)	-----								
Consensus	(107)	GTMVEIK								

Positives: 86.7% Identity: 85.0%

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FIGURE 24

positives: 79.8% identity: 77.3%

FIGURE 25

		Section 1				
	(1)	1	10	20	30	40 53
A15-365_LC	(1)	DIQMTQSPSSLSASVGDRVTITCOASQDI NYLNWYQQKPGKAPKLLIYDASN				
08	(1)	DIQMTQSPSSLSASVGDRVTITCOASQDI NYLNWYQQKPGKAPKLLIYDASN				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCOASQDI NYLNWYQQKPGKAPKLLIYDASN				
		Section 2				
	(54)	54	60	70	80	90 106
A15-365_LC	(54)	LETGVPSRFSGSGSGTDFTFTIS LQPEDIAITYCQOYD LP				
08	(54)	LETGVPSRFSGSGSGTDFTFTIS LQPEDIAITYCQOYD LP				
Consensus	(54)	LETGVPSRFSGSGSGTDFTFTIS LQPEDIAITYCQOYD LP				
		Section 3				
	(107)	107				
A15-365_LC	(107)	K				
08	(96)	-				
Consensus	(107)					
		Positives: 86.0% Identity: 86.0%				

FIGURE 26

								Section 1
	(1)	1	10	20	30	40	53	
A15-6.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSY						
VH3-30	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIVSY						
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIVSY						
								Section 2
	(54)	54	60	70	80	90	106	
A15-6.1_HC	(54)	DGSNKYYADSVKGRFTISRDN SKNTLY LQMNSIPRAEDTAVYYCAR SIFGVVID						
VH3-30	(54)	DGSNKYYADSVKGRFTISRDN SKNTLY LQMNSI RAEDTAVYYCAR -----						
Consensus	(54)	DGSNKYYADSVKGRFTISRDN SKNTLY LQMNSI RAEDTAVYYCAR						
								Section 3
	(107)	107	122					
A15-6.1_HC	(107)	YGMDVWGQGTTVTVSS						
VH3-30	(99)	-----						
Consensus	(107)							

positives: 80.3% identity: 79.5%

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FIGURE 27

										Section 1
	(1)	1	10	20	30	40	54			
A15-6.1 LC	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI RNYLAWYQQNGPKVKKLLIYAASLT								
A20	(1)	DTQMTQSPSSLSASVGDRTITCRASQGI SNYLAWYQQKPKGVKKLLIYAASLT								
Consensus	(1)	DIQMTQSPSSLSASVGDRTITCRASQGI NYLAWYQQ PGKVKLLIYAASLT								
										Section 2
	(55)	55	60	70	80	90	107			
A15-6.1 LC	(55)	QSGVPSRFSGSGSGTDFTLTITSSLPEDVATYYCQKFSPTFTFGPGTKVDIS								
A20	(55)	QSGVPSRFSGSGSGTDFTLTITSSLPEDVATYYCQKNSAE-----								
Consensus	(55)	QSGVPSRFSGSGSGTDFTLTITSSLPEDVATYYCQKFSPT								

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FIGURE 28

Section 1									
	(1)	1	10	20	30	40	50	60	53
A15-6.12_HC	(1)	QVQL EQSGPGLVKPSEETLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYI							
VH4-31	(1)	QVQLQESGPGGLVKPSEOTLSLTCTVSGGSISSGGYHWSWIRQHPGKGLEWIGYI							
Consensus	(1)	QVQL SGPGLVKPS TLSLTCTVSGGSISSG YHWSWIRQHPGKGLEWIGYI							
Section 2									
	(54)	54	60	70	80	90	100	110	106
A15-6.12_HC	(54)	YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRY							
VH4-31	(54)	YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR-----							
Consensus	(54)	YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR							
Section 3									
	(107)	107	117						
A15-6.12_HC	(107)	WGQGTLLVTVSS							
VH4-31	(100)	-----							
Consensus	(107)								

positives: 81.2% identity: 77.6%

FIGURE 29

										Section 1
	(1)	1	10	20	30	40	53			
L2	(1)	EIVMTQSPATLSVSPGERATLSCRASQSVESNLAHYQQRPGQAPRLITFGAST								
A15-6.12_LC	(1)	EIVMTQSPATLSVSPGERATLSCRASQSVESNLAHYQQRPGQAPRLITFGAST								
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRASQSI S N AWYQQKPGQAPRLITFGAST								
										Section 2
	(54)	54	60	70	80	90	106			
L2	(54)	RATGIPARFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWP-----								
A15-6.12_LC	(54)	RATGIPARFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWPERTFGQGTKVEI								
Consensus	(54)	RATGIPARFSGSGSGTEFTLTITSSLSQSEDFAVYYCQYNNWP								
										Section 3
	(107)	107								
L2	(96)	-								
A15-6.12_LC	(107)	K								
Consensus	(107)									

Positives: 96.9% Identity: 85.0%

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		Section 1					
	(1)	1	10	20	30	40	53
A15-6.2_HC	(1)	QVQLQESGPGGLVLRPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYY					
VH4-59	(1)	QVQLQESGPGGLVLRPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYY					
Consensus	(1)	QVQLQESGPGGLVLRPSETLSLTCTVSGGSISSYYMSWIRQPPGKGLEWIGYIYY					
		Section 2					
	(54)	54	60	70	80	90	106
A15-6.2_HC	(54)	TGNTYYNPSLKSRTVISVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPD					
VH4-59	(54)	SGSTNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCAR-----					
Consensus	(54)	SG T YNPSLKSRTVISVDTSKNQFSLKL SVTAADTAVYYCAR					
		Section 3					
	(107)	107	121				
A15-6.2_HC	(107)	AFDIWGQGTMTVSVSS					
VH4-59	(98)	-----					
Consensus	(107)						

positives: 77.7%	identity: 75.2%
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FIGURE 31

Section 1

	(1)	10	20	30	40	54
A15-6.2_LC	(1)	DI VMTQSPISLSPVIRGEPASISCRSSQSLITSGNNNYLDNYLQKPGQSPQLLIY				
A19	(1)	DI VMTQSPISLSPVIRGEPASISCRSSQSLITSGNGYNYLDNYLQKPGQSPQLLIY				
Consensus	(1)	DIVMTQSPLSLPVIRGEPASISCRSSQSLITSGNYLDNYLQKPGQSPQLLIY				

Section 2

	(55)	55	60	70	80	90	108
A15-6.2_LC	(55)	LGSNRASGVDPDRFSGSGSGTDFTLKISRVEADLVGYYCMQALQTPLTFGGGGTK					
A19	(55)	LGSNRASGVDPDRFSGSGSGTDFTLKISRVEADLVGYYCMQALQTPE-----					
Consensus	(55)	LGSNRASGVDPDRFSGSGSGTDFTLKISRVEADLVGYYCMQALQ P					

Section 3

	(109)	109	112
A15-6.2_LC	(109)	VEIK	
A19	(101)	----	
Consensus	(109)		

positives: 85.7% identity: 83.9%

FIGURE 32

										Section 1							
	(1)	1	10	20	30	40	50	60	70	53							
A15-6.9_HC	(1)	QVQLEQSGPGLVKPSETLSLTCTVSGGSISGGTYHNSWIRQHPGKGLEWIGYI															
VH4-31	(1)	QVQLEQSGPGLVKPSETLSLTCTVSGGSISGGTYHNSWIRQHPGKGLEWIGYI															
Consensus	(1)	QVQLSGPGLVKPSTLSLTCTVSGGSISG YHWSWIRQHPGKLEWIGYI															
										Section 2							
	(54)	54	60	70	80	90	100	110	120	106							
A15-6.9_HC	(54)	YYSGSTYHNP SLKSRITISVDTSKNQFSLKLSSTVAADTAVYYCARGGDGYRY															
VH4-31	(54)	YYSGSTYHNP SLKSRITISVDTSKNQFSLKLSSTVAADTAVYYCAR-----															
Consensus	(54)	YYSGSTYHNP SLKSRITISVDTSKNQFSLKLSSTVAADTAVYYCAR															
										Section 3							
	(107)	107	117														
A15-6.9_HC	(107)	WGQGTLLTVSS															
VH4-31	(100)	-----															
Consensus	(107)																

positives: 61.2% identity: 77.8%

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FIGURE 33

Section 1							
	(1)	1	10	20	30	40	54
A15-6.9_LC	(1)	EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQOKPGQAPRLILFGASTR					
L2	(1)	EIVMTQSPATLSVSPGERATLSCRASQSISSNLAWYQOKPGQAPRLILFGASTR					
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRASQSISS N AWYQOKPGQAPRLILFGASTR					
Section 2							
	(55)	55	60	70	80	90	107
A15-6.9_LC	(55)	ATGIPARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWERTFGQGTKVEIK					
L2	(55)	ATGIPARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWF-----					
Consensus	(55)	ATGIPARFSGSGSGTEFTLTISLSQSEDFAVYYCQYNNWF					

positives: 86.9% identity: 85.0%

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FIGURE 34

		(1)	1	10	20	30	40	53	Section 1
A15-6.11_HC	(1)	QVQLQESGGPGLVKPSQTLSLTCTVSGGSISGGTYHWSWIRQHPGKGLEWIGYI							
VH4-31	(1)	QVQLQESGGPGSLVKPSQTLSLTCTVSGGSISGGGYHWSWIRQHPGKGLEWIGYI							
Consensus	(1)	QVQLQESGPGLVKPSQTLSLTCTVSGGSISGGYHWSWIRQHPGKGLEWIGYI							
		(54)	54	60	70	80	90	106	Section 2
A15-6.11_HC	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKY							
VH4-31	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----							
Consensus	(54)	YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR							
		(107)	107	117					Section 3
A15-6.11_HC	(107)	WGQGTLVTVSS							
VH4-31	(100)	-----							
Consensus	(107)								

positives: 83.8%	identity: 82.9%
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FIGURE 35

		Section 1					
	(1)	1	10	20	30	40	53
A15-6.11_LC	(1)	EIVMTQSPATLSVSPGERATLSCRAEQSVSNLAWYQOKPGQAPRLIIYGAST					
L2	(1)	EIVMTQSPATLSVSPGERATLSCRAEQSVSNLAWYQOKPGQAPRLIIYGAST					
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRAEQSVSNLAWYQOKPGQAPRLIIYGAST					
		Section 2					
	(54)	54	60	70	80	90	106
A15-6.11_LC	(54)	RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPERTFGQGTKVEI					
L2	(54)	RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPERTFGQGTKVEI					
Consensus	(54)	RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQYNNWPERTFGQGTKVEI					
		Section 3					
	(107)	107					
A15-6.11_LC	(107)	K					
L2	(96)	-					
Consensus	(107)						

positives: 67.9% identity: 87.9%

FIGURE 36

CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
A15-3.10	DP-714-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.22	DP-654-31	0	GAGAGA	9	GGGAGATGG	-	-	-	-	-	JH4B	-4	CTTTGA
A15-3.27	DP-714-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.45	DP-141-18	0	GAGAGA	6	AACTAA	D3-10	12	GGTTCGGGGAGT	2	CC	JH3B	-9	ACTACT
A15-3.65	DP-654-31	0	GAGAGA	8	TCGGGAAA	D6-13	8	CAGCTGGT	4	TTTT	JH5A	-11	GACTAC
A15-6.1	DP-493-30	3	GCGAGA	1	T	D3-3	18	CGATTTTGGAGTGGTTA	3	TCG	JH6B	-12	ACTACG
A15-6.2	DP-714-59	0	GAGAGA	7	TCCAGGC	D6-19	11	CAGTGGCTGGT	5	CCCTG	JH3B	0	ATGCTT
A15-6.9	DP-654-31	1	CGAGAG	3	GGG	D6-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG
A15-6.11	DP-654-31	1	CGAGAG	3	GGG	D5-24	13	GAGATGGCTACAA	2	GT	JH1	-16	ACTGGG
A15-6.12	DP-654-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG

CLONE	vk	#del	vk end	#n	N SEQ	JK	#del	JK end
A15-3.10	02/012DPK	0	CCCTCC	9	GGAGTGCAG	JK2	-7	TTTTGG
A15-3.22	A30	3	TTACCC	0	0	JK4	0	GCTCAC
A15-3.27	A30	3	TTACCC	0	0	JK1	0	GTGGAC
A15-3.45	B3/DPK24	1	TCCCTC	3	GGT	JK1	-5	CGTTCG
A15-3.65	08/018DPK	1	TCCCTC	0	0	JK4	-2	TCACITTC
A15-6.1	A20/DPK4	3	GTCCCC	0	0	JK3	0	ATTCAC
A15-6.2	A31A19DPK	1	TCCCTC	0	0	JK4	-2	TCACITTC
A15-6.9	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.11	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.12	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT